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M. K. J. van't Hof-Grootenboer et al., Using SW model

Run on:	September 10, 2002, 13:02:35	Search time 11.92 Seconds (without alignments)
		643.415 Million cell updates/sec

111101	US 09-848-915-1
Footnote score:	1000
Reference:	1 MEDLINE/SCIENCE/ARTICLE.....GOLVERI,KIDANESEI PIPATDI 195

Storage table: BLDSIM62
 captop 10.0 , capext. 0.5

Selected: 105224 seqs, 36719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum PR Seq length: 2000000000

Post-processed:	Minimum Match: 0%
	Maximum Match: 100%
Listing:	Listing: 45 summaries

[illegible]

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Accession	Species	Match	Length	DB	Description
1	94.5	9.3	2318	NTF_MOUSE	561982 mus musculus
2	92.8	9.2	583	LAM_XENLA	110999 xenopus lae
3	92.5	9.2	874	LAM_XENLA	123420 xenopus lae
4	88	8.9	859	RASO_PRRHO	058687 pyrococcus
5	84.5	8.4	581	Y208_PRRHO	051226 borrelia bu
6	84.5	8.4	1390	CYAO_KAT	026269 rattus nor
7	84	8.4	1478	CLH_DROME	029742 drosophila
8	84	8.4	2111	MYO1_DROME	046541 homo sapien
9	81.5	8.2	828	SYL_RITRO	094811 rickettsia
10	81	8.1	1134	TFX3_HOMAN	075153 homo sapien
11	80	8.0	474	TFX4_HOMAN	090441 homo sapien
12	80	8.0	739	CEPB_ARAB	091819 arabidopsis
13	80	8.0	697	CYAO_HOMAN	008442 homo sapien
14	80	8.0	1162	TFX2_HOMAN	095602 homo sapien
15	80	8.0	1233	DNGL_HOMAN	040088 homo sapien
16	80	8.0	2511	NTG1_RAT	007068 rattus norv
17	79	7.9	622	IOF3_SCHRO	061136 schizosacch
18	79	7.9	2544	R312_XENLA	017163 xenopus lae
19	79	7.9	2581	NTG1_MOUSE	011705 mus musculu
20	77	7.8	439	RFA1_HOMO1	024173 escherichia
21	77	7.7	420	STH_STAAM	024142 staphylococ
22	77	7.7	504	DNTP_SALTY	040783 salmonella
23	73	7.2	1938	MYS_ABOIR	024733 acetyliposac
24	73	7.2	1043	PEF3_YEAST	053788 saccharomyc
25	73	7.2	1045	SOS_FERTY	049031 beta vulgaris
26	71.5	7.2	1687	YHBA_SCHRO	092355 schizosacch
27	71.5	7.2	819	LON_XENLA	092914 chlamydia f
28	71.5	7.2	1325	Y409_MYCIN	025314 mycoplasma
29	71.5	7.2	1804	YFAT2_YEAST	043583 saccharomyc
30	71.5	7.2	421	Y306_PRRHO	064202 mycobacteri
31	71.5	7.2	504	DNTP_ECOLI	015723 escherichia
32	71.5	7.2	504	DNTP_ESGTE	059435 escherichia
33	71.5	7.2	504	DNTP_SHILO	059827 shigella bo

45	73	7.3	2022	1	ANF1_UNCVO	homo sapiens	121240	homo sapiens
44	73	7.3	2017	1	MYSLN_PRODM	mus musculus	999420	mus musculus
43	73	7.3	1171	1	DIA3_MOUSE	mus musculus	999420	mus musculus
42	73	7.3	950	1	Y511_RICPR	yeast	950466	yeast
41	73	7.3	899	1	RH_RAT	rattus norvegicus	345666	rattus norvegicus
40	73	7.3	578	1	V022_PEWY	homo sapiens	142646	homo sapiens
39	73	7.3	284	1	TPM1_HUMAN	homo sapiens	142646	homo sapiens
38	73.5	7.3	3655	1	YABH5_HUMAN	homo sapiens	910604	homo sapiens
37	73.5	7.3	2704	1	BVAL_HUMAN	homo sapiens	934248	homo sapiens
36	73.5	7.3	971	1	GF041_HUMAN	homo sapiens	934248	homo sapiens
35	75	7.5	3433	1	UTROB_HUMAN	homo sapiens	1469346	homo sapiens
34	75	7.5	684	1	SK11_HUMAN	homo sapiens	1469346	homo sapiens

ALIGNMENT

	RESULT	1
ID	NTRC_MOUSE	STANDARD; PRT, 2318 AA.
AC	Q61982;	
FT	01-NOV-1997 (Rel. 35, Created)	
FT	01-NOV-1997 (Rel. 35, Last sequence update)	
FT	16-OCT-2001 (Rel. 40, last annotation update)	
DE	Neurogenic locus notch 3 protein.	
CN	NOTCH3.	
CS	Mus musculus (Mouse).	
OC	Eumetazoa; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Scurionodonta; Muridae; Mus.	
OX	NH_TaxID=10090.	
RN	11	
PD	SEQUENCE FROM N.A.	
RC	STRAIN ICR X SWISS WEBSTER;	
RX	MEDLINE=55001556; PubMed-7918097;	
RA	Ladell L M., Dalstrand J., Ladell U.;	
RT	"The novel Notch homologue mouse Notch 3 lacks specific epithelial growth factor repeats and is expressed in proliferating neuroepithelium."	
XT	neuroepithelium; ?	
CL	Mesh. Desc. 46312+316(1994);	
FC	-1- FUNCTION: NOTCH 1, 2 AND 3 PLAY A COMBINATIONAL ROLE DURING VALTIOUS CELL FATE DECISIONS AND MODULATE AT LEAST ONE IN THE DEVELOPING CNS AND PROBABLY OTHER TISSUES IN THE EMBRYO.	
CC	-1- TISSUE SPECIFICITY: PROLIFERATING NEUROEPITHELIAL.	
CC	-1- DEVELOPMENTAL STAGE: CNS DEVELOPMENT.	
CC	-1- SIMILARITY: CONTAINS 34 EGF LIKE REPEATS.	
CC	-1- SIMILARITY: CONTAINS 4 INTERDIGITAL REPEATS.	
CC	-1- SIMILARITY: CONTAINS 5 ANK REPEATS.	
CC	This SWISS PRO entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, abused or used for commercial entities requires a license agreement (http://www.ebi.ac.uk/ebis/tss/extras/copyright.html) or send an email to license@ebi.ac.uk .	
CC	EMBL: X74760; CAA52776.1; -	
DR	HSSP: P00740; ILRX.	
DR	MED: MG159460; Notch3.	
DR	TrEMBL: IP000710; ANK.	
DR	InterPro: IP000192; ASX_hydroxyl.	
DR	InterPro: IP000561; EGF-like.	
DR	InterPro: IP000742; EGF_2.	
DR	InterPro: IP001881; EGF_Ga.	
DR	InterPro: IP001438; EGF_11.	
DR	InterPro: IP000800; Notch.	
DR	Pfam: PF00023; ank_6.	
DR	Pfam: PF00008; EGF_34.	
DR	Pfam: PF00066; notch_3.	
DR	PRINTS: PR00010; EGFIMOD.	
DR	PRINTS: PR01452; NOTCH.	
DR	SMART: SM00248; ANK_5.	
DR	SMART: SM00179; EGF_CA; 19.	

[illegible]

[illegible]

QUERY MATCH: 8-28; SCORE 81.5; DP 1; LENGTH 828;
BEST LOCAL SIMILARITY: 19.5%; FROM NO. 9-6
MATCHES: 44; CONSERVATIVE: 32; MISMATCHES: 81; INDELS: 27; GAPS:

QY LEAATGSSLLDNACAPPAVLIPPELKEPPNVALEPDAAAATPVLFALDEPAISITSTYLE 88
DDB LERMTALFSLKRRERSLNKLRLNLHLFKLVAVGLEEDLSNAIAMDLTIANIVE 708
QY DCRVTEELHGLLYCHRRSELEEGGLTGGEELIKNSRETYEPLTRAEETR 146
DDB TDKPTDWFTKYCPN-----VLVALINEPPIHEEIQW-----KIADKERIYSKV 795
QY IAF-----PAVVTSVCNTDSPTSPERFSMSQLGLWKRIAKSKSL 189
DDB PAFEPHSILLIEYSTVMAYGVNKAIDRDYLAIVDPSVDVCLVNLTGSVKDTL 808

RESULT: 10
TFX_HUMAN
ID_TFX_HUMAN STANDARD PRG: 1134 AA.
AC 075154;
DT 30-MAY-2000 (Rel. 49, Created)
DI 30 MAY 2000 (Rel. 49, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DEF putative eukaryotic translation initiation factor 3 subunit (eIF 3) (Fragment).
GN KIAA0664.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euarchontia; Primates; Catarrhini; Hominoidea; Homin.
OX NCBI_Taxid=9606;
RN R1
RS SEQUENCE FROM N.A.
RC ISSUES: Brain.
RA MEHLINE-98403880; PubMed:9734811;
FA ISLIKAW K. L., Nakano T., Sugiyama M., Miyajima N., Tanaka A.,
KO Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X,
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
RL DNA ROS. 5(169-176)(1998);
GC FUNCTION: BELONGS TO THE 40S RIBOSOME AND PROTECTS THE RETURN OF
+ PEPTIDE BOND AND BINDS (BY STIMULATORY).
CC SUBUNIT EIF 3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS (BY
SIMILARITY).
CC + SIMILARITY: BELONGS TO THE EIF 3-LIKE FAMILY.

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Entry Acc: P57641; AAA31639.1;
KW Hypothetical protein; Initiation factor; protein biosynthesis.
FT NO_BORDER 1
SD SPOURIN 1134 AA; 127415 MW; 5940163.68% IDV91 CWR64;

Query Match:		8.1%	Score 81,	E-Value 11.64
Best Local Similarity:	23.5%	Frag. No. 16		
Matches:	48;	Conservative:	41;	Mismatches: 6%; Indels: 6%; Gaps: 11

```

6 SVLPFGMLAPRPEN ALTLIAVAGSLTPVAMPVDS WQPKIHVVKH GL
111 111 111 111 111 111 111 111
759 SLKTVGLVEVEESHDFAT -----EEVENFEVVRVP
62 QAAAATAALLAQASAASLTLTLTFLTAATVTTLTNYVFPHLTHLTTASS LT
111 111 111 111 111 111 111 111 111 111 111 111 111
749 -KASIAEFHPDGARKVGQCFPR LSQIIEMAIADRNV --CAHVETQVTELD 850
    
```


Query Match	Similarity	Score	Length	Gap
38	Connective	43	Mismatch 79	Indel 15
39	Connective	43	Mismatch 79	Indel 15
40	Connective	43	Mismatch 79	Indel 15
41	Connective	43	Mismatch 79	Indel 15
42	Connective	43	Mismatch 79	Indel 15
43	Connective	43	Mismatch 79	Indel 15
44	Connective	43	Mismatch 79	Indel 15
45	Connective	43	Mismatch 79	Indel 15
46	Connective	43	Mismatch 79	Indel 15
47	Connective	43	Mismatch 79	Indel 15
48	Connective	43	Mismatch 79	Indel 15
49	Connective	43	Mismatch 79	Indel 15
50	Connective	43	Mismatch 79	Indel 15
51	Connective	43	Mismatch 79	Indel 15
52	Connective	43	Mismatch 79	Indel 15
53	Connective	43	Mismatch 79	Indel 15
54	Connective	43	Mismatch 79	Indel 15
55	Connective	43	Mismatch 79	Indel 15
56	Connective	43	Mismatch 79	Indel 15
57	Connective	43	Mismatch 79	Indel 15
58	Connective	43	Mismatch 79	Indel 15
59	Connective	43	Mismatch 79	Indel 15
60	Connective	43	Mismatch 79	Indel 15
61	Connective	43	Mismatch 79	Indel 15
62	Connective	43	Mismatch 79	Indel 15
63	Connective	43	Mismatch 79	Indel 15
64	Connective	43	Mismatch 79	Indel 15
65	Connective	43	Mismatch 79	Indel 15
66	Connective	43	Mismatch 79	Indel 15
67	Connective	43	Mismatch 79	Indel 15
68	Connective	43	Mismatch 79	Indel 15
69	Connective	43	Mismatch 79	Indel 15
70	Connective	43	Mismatch 79	Indel 15
71	Connective	43	Mismatch 79	Indel 15
72	Connective	43	Mismatch 79	Indel 15
73	Connective	43	Mismatch 79	Indel 15
74	Connective	43	Mismatch 79	Indel 15
75	Connective	43	Mismatch 79	Indel 15
76	Connective	43	Mismatch 79	Indel 15
77	Connective	43	Mismatch 79	Indel 15
78	Connective	43	Mismatch 79	Indel 15
79	Connective	43	Mismatch 79	Indel 15
80	Connective	43	Mismatch 79	Indel 15
81	Connective	43	Mismatch 79	Indel 15
82	Connective	43	Mismatch 79	Indel 15
83	Connective	43	Mismatch 79	Indel 15
84	Connective	43	Mismatch 79	Indel 15
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91	Connective	43	Mismatch 79	Indel 15
92	Connective	43	Mismatch 79	Indel 15
93	Connective	43	Mismatch 79	Indel 15
94	Connective	43	Mismatch 79	Indel 15
95	Connective	43	Mismatch 79	Indel 15
96	Connective	43	Mismatch 79	Indel 15
97	Connective	43	Mismatch 79	Indel 15
98	Connective	43	Mismatch 79	Indel 15
99	Connective	43	Mismatch 79	Indel 15
100	Connective	43	Mismatch 79	Indel 15

[illegible][illegible]



